

## SCIENCE'S COMPASS

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### References and Notes

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9. We thank D. Birx and F. McCutchan of the U.S. Army and the Henry M. Jackson Foundation; J. Bradac of the National Institute of Allergy and Infectious Dis-

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### Traces of Symmetric Chaos

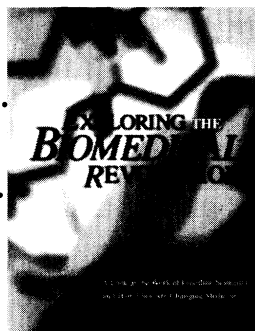
The Editors' Choice selection entitled "Chaos underlying order" (Phillip D. Szuro-mi, 18 Feb., p. 1169) describes the work of Encinas-Sanz *et al.* (1), in which regular pat-terns arise when a system that is chaotic on short time scales (a few nanoseconds) is ob-served over longer time scales (around 100 nanoseconds). Their system is a laser beam, the nonchaotic dynamics of which is well known to exhibit many symmetric patterns. This fact, together with the reference to "rolls" in the long-term pattern, suggests that this effect is probably an example of "symmetric chaos," in which a symmetric dynamical system has a chaotic attractor (2). This attractor usually has symmetry, al-though not necessarily the same symmetry as the overall system because of the possibil-ity that the symmetry could be broken. Short-term "snapshots" of the state of the system appear unstructured because short-term observations explore too small a region of the attractor for the overall symmetry to become apparent. Longer-term observations

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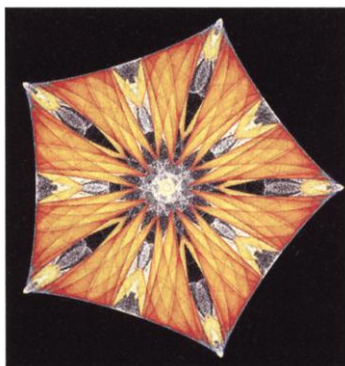
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in effect average or sum instantaneous observations over a subset of the attractor that is large enough to reveal the global symmetry. In mathematical models, the relevant symmetry arises through such things as the choice of domain for the model and its boundary conditions. In experiments, symmetry derives from the design of the apparatus and the underlying symmetry of physical laws.

Within the nonlinear dynamics community, the concept of symmetric chaos was formulated in 1988 by Chossat and Golubitsky (3, 4) and has been extensively studied since (5–7). To date, the main experimental verification is that of Gluckman *et al.* (8) for the Faraday experiment, in which a thin layer of fluid in a dish is vibrated vertically. At suitable frequencies, the instantaneous state appears chaotic. However, the symmetry of the dish affects the symmetry of the underly-

ing chaotic attractor, and this effect can be revealed by averaging the observed patterns over time. Chaos notwithstanding, the averaged observation is not featureless. In a square dish, the averaged pattern is a square-symmetric checkerboard of waves parallel to the sides of the dish. In a circular dish, the average is a “target pattern” of concentric circular rolls.



An example of symmetric chaos in a mathematical model.

Ian Stewart

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## Scientists at Brookhaven

For the News Focus article “Meltdown on Long Island” by Andrew Lawler (25 Feb., p. 1382), I did not say to Lawler that “The whole lab is corrupt,” in reference to Brookhaven National Laboratory. Although the STAR (Standing for Truth About Radiation) Foundation has had the greatest reservations about the truthfulness and good faith of those charged with overseeing Brookhaven’s nuclear capabilities, we nonetheless recognize the good scientific work being done by many research scientists there. It would be unfair to contaminate them all, if you will, with the same brush.

Alec Baldwin\*

c/o STAR Foundation, 66 Newtown Lane, East Hampton, NY 11937, USA

\* Board co-chairman

#### Editors’ note

Baldwin’s comment was shortened during editing. The full quote was, “The whole lab as an institution is corrupt.”

#### CORRECTIONS AND CLARIFICATIONS

News Focus: “A reluctant warrior” by Jocelyn Kaiser (18 Feb., p. 1190). Gene Likens’ age should have been 65, not 67.

CREDIT: MIKE FIELD AND MARTY GOLUBITSKY, SYMMETRY IN CHAOS (1992)

### Short Course in Computational Molecular Biology



Eric P. Newman Educational Center  
Washington University in St. Louis

July 10-14, 2000

**Objectives:** The faculty of Washington University’s computational molecular-biology program offers a challenging, intensive course covering material from our regular graduate course on computational biology in a format that is accessible to working scientists. Participants will become familiar with the theory and practice of molecular sequence analysis and are offered sessions on programming in PERL. Participants should be accustomed with basic molecular biology and mathematics to the level of college calculus, but do not require programming skills or higher-level computer science. The course is targeted to students at the level of a first or second year doctoral candidate and addresses professional scientists in molecular biology or biotechnology. The aim of the course is to provide an appreciation for how and why different analytic approaches are used, their capabilities and their limitations. We emphasize the use of public domain software tools rather than focusing on a specific commercial package.

**Syllabus:** 5-day course with 6 hours of lectures each day (3 hrs. in the morning and 3 hrs in the afternoon).

- Probability and statistics, model based data analysis, HMMs, gene modeling and gene finding
- Protein models, threading, dynamic programming, optimal and suboptimal RNA alignment and folding
- Information measures, Karlin-Altschul statistics, Sum statistics, gapped BLAST, database searching
- Multiple sequence alignment, Generalized dynamic programming, Phylogeny and molecular evolution
- Physical mapping, Data clustering, and the inference of classifications, Expression data analysis

One of the two offered PERL programming sessions is targeted to professional software developers and the other two to scientists with a limited background in computer programming. All participants are encouraged to bring a laptop computer (Windows/Intel) for use in the programming sessions. A CD-ROM containing course lecture notes, problem sets, programming exercises, public domain software and reference material will be distributed.

**Instructors:** David States (course master) Institute for Biomedical Computing  
Warren Gish Department of Genetics  
Volker Nowotny Institute for Biomedical Computing  
Gary Stormo Department of Genetics  
Michael Zuker Institute for Biomedical Computing

Graduate students from the Institute for Biomedical Computing will fill in as Teaching Assistants.

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